

AMENDMENTS TO THE CLAIMS

1.-37. (Canceled)

38. (Previously presented) The method of claim 111 wherein the nucleic acid target is RNA.

39. (Previously presented) The method of claim 111 wherein the nucleic acid target comprises RNA and one or more deoxynucleotides.

40.-94. (Canceled)

95. (Currently Amended) The method of claim 111, wherein each test ~~compound~~ ligand is an oligonucleotide.

96. (Canceled)

97. (Currently Amended) The method of claim 111, wherein each test ~~compound~~ ligand is a small molecule.

98. (Previously presented) The method of claim 38, wherein the RNA comprises a molecular interaction site present in two or more distinct taxonomic species.

99. (Currently Amended) The method of claim 112, wherein each test ~~compound~~ ligand is an oligonucleotide.

100. (Canceled)

101. (Previously presented) The method of claim 112, wherein the nucleic acid target is RNA.

102. (Canceled)

103. (Previously presented) The method of claim 101, wherein the RNA comprises a molecular interaction site present in two or more distinct taxonomic species.

104. (Currently Amended) The method of claim 112, wherein each test ~~compound~~ ligand is a small molecule.

105.-108. (Canceled)

109. (Previously presented) The method of claim 38, wherein the RNA comprises a molecular interaction site.

110. (Previously presented) The method of claim 101, wherein the RNA comprises a molecular interaction site.

111. (Currently Amended) A method comprising

- (a) selecting a nucleic acid target comprising at least one loop, bulge, kink, stem structure, or mismatched base pair, wherein the mass of the nucleic acid target is known;
- (b) forming a first complex comprising a standard binding compound and the nucleic acid target;
- (c) combining the first complex with a mixture of two or more test ~~compounds~~ ligands under competitive binding conditions to allow formation of at least one test compound-nucleic acid-target complex, wherein the mass of each test ~~compound~~ ligand is known;
- (d) subjecting the combination of step (c) to mass spectrometry;
- (e) collecting mass spectral data for the combination, wherein the mass spectral data comprises an ion abundance and a mass to charge ratio for an ion of at least one test ~~compound-nucleic acid-target~~ second complex;
- (f) calculating the mass of ~~at least one test compound-nucleic acid-target~~ at least one second complex; and
- (g) ~~calculating the difference between the known mass of the nucleic acid target and at least one test compound-nucleic acid-target complex to determine~~ determining

the identity of the one or more test compounds ligand compound bound in the at least one test compound-nucleic acid target second complex, based on the masses of the test ligands and the mass of the second complex.

112. (Currently Amended) A method comprising

- (a) forming a first complex comprising a nucleic acid target and a standard binding compound, wherein the nucleic acid target comprises at least one loop, bulge, kink, stem structure, or mismatched base pair, wherein the mass of the standard binding compound is known;
- (b) subjecting the first complex to mass spectrometry;
- (c) collecting mass spectral data for the first complex, wherein the mass spectral data comprises an ion abundance and a mass to charge ratio for an ion of the complex;
- (d) combining the first complex with a mixture of two or more test ~~compounds~~ ligands under competitive binding conditions ~~to allow formation of at least one test compound-nucleic acid target complex~~, wherein the mass of each test ~~compound~~ ligand is known;
- (e) subjecting the combination of step (d) to mass spectrometry;
- (f) collecting mass spectral data for the combination, wherein the mass spectral data comprises an ion abundance and a mass to charge ratio for an ion of at least one ~~test compound-nucleic acid target~~ second complex;
- (g) calculating the mass for the first complex and for ~~at least one test compound-nucleic acid target~~ the second complex; and
- (h) calculating the difference between the mass of the first complex and ~~at least one test compound-nucleic acid target~~ the second complex to determine the identity of the at least one test compound ligand bound in the ~~at least one test compound-nucleic acid target~~ second complex.

113. – 114. (cancelled)

115. (Previously presented) The method of claim 111, wherein the binding affinity of the standard binding compound for the nucleic acid target is known.

116. (Currently Amended) The method of claim 115, comprising using the ion abundance data collected in step (e) to calculate the relative concentrations of the first complex and the ~~at least one test compound-nucleic acid target~~ second complex.

117. (Currently Amended) The method of claim 116 comprising calculating the binding affinity of the a bound test compound for the nucleic acid target.

118. (Previously presented) The method of claim 112, wherein the binding affinity of the standard binding compound for the nucleic acid target is known.

119. (Currently Amended) The method of claim 118, comprising using the ion abundance data collected in step (f) to calculate the relative concentrations of the first complex and the ~~at least one test compound-nucleic acid target~~ second complex.

120. (Currently Amended) The method of claim 119 comprising calculating the binding affinity of the bound test ~~compounds~~ ligand for the nucleic acid target.